

10/534238
JC17 Rec'd PCT/PTO 06 MAY 2005

Sequence listing

<110> Institute of Cell Biophysics RAS

<120> Antioxidant Pharmaceutical Compound, Method for Producing Polypeptide and Method of Cure

<130>

<150> RU 2002129774

<151> 2002.11.10

<160> 6

<210> 1

<211> 224

<212> cDNA-mRNA

<213> Homo sapiens

```

<400> cggttgcttg ctgtccacgc ggcgccccct catcacgcgc gcc atg ccc gga ggt ctg 58
      Met Pro Gly Gly Leu
      1 5
      ctt ctc ggg gac gtg gct ccc aac ttt gag gcc aat acc acc gtc ggc 106
      Leu Leu Gly Asp Val Ala Pro Asn Phe Gly Ala Asn Thr Thr Val Gly
      10 15 20
      cgc atc cgt ttc cac gac ttt ctg gga gac tca tgg ggc att ctc ttc 154
      Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser Trp Gly Ile Leu Phe
      25 30 35
      tcc cac cct cgg gac ttt acc cca gtg tgc acc aca gag ctt ggc aga 202
      Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr Thr Glu Leu Gly Arg
      40 45 50
      gct gca aag ctg gca cca gaa ttt gcc aag agg aat gtt aag ttg att 250
      Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg Asn Val Lys Leu Ile
      55 60 65
      gcc ctt tca ata gac agt gtt gag gac cat ctt gcc tgg agc aag gat 298
      Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu Ala Trp Ser Lys Asp
      70 75 80 85
      atc aat gct tac aat tgt gaa gag ccc aca aag tta cct ttt ccc 346
      Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu Lys Leu Pro Phe Pro
      90 95 100
      atc atc gat gat agg aat cgg gag ctt gcc atc ctg ttg ggc atg ctg 394
      Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile Leu Leu Gly Met Leu
      105 110 115
      gat cca gca gag aag gat gaa aag ggc atg cct gtg aca gct cgt gtg 442
      Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro Val Thr Ala Arg Val
      120 125 130

      gtg ttt gtt ttt ggt cct gat aag aag ctg aag ctg tct atc ctc tac 490
      Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys Leu Ser Ile Leu Tyr
      135 140 145
      cca gct acc act ggc agg aac ttt gat gag att ctc agg gta gtc atc 538
      Arg Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile Leu Arg Val Val Ile
      150 155 160 165
      tct ctc cag ctg aca gca gaa aaa agg gtt gcc acc cca gtt gat tgg 586
      Ser Leu Gln Leu Thr Ala Glu Lys Arg Val Ala Thr Pro Val Asp Trp
      170 175 180
      aag gat ggg gat agt gtg atg gtc ctt cca acc atc cct gaa gaa gaa 634
      Lys Asp Gly Asp Ser Val Met Val Leu Pro Thr Ile Pro Glu Glu Glu
      185 190 195
      gcc aaa aaa ctt ttc ccg aaa gga gtc ttc acc aaa gag ctc cca tct 682

```

Ala	Lys	Lys	Leu	Phe	Pro	Lys	Gly	Val	Phe	Thr	Lys	Glu	Leu	Pro	Ser	
		200					205					210				
ggc	aag	aaa	tac	ctc	cgc	tac	aca	ccc	cag	cct						715
Gly	Lys	Lys	Tyr	Leu	Arg	Tyr	Thr	Pro	Gln	Pro						
	215					220										

<110> Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry Russian Academy of Sciences, Institute of Cell Biophysics RAS.

<120> Recombinant plasmid DNA pET23-a(+)/PrxVIhumΔ178 encoding N- terminal fragment of human peroxyredoxin VI and a bacterial strain *Escherichia coli* I pET23-a(+)/PrxVIhumΔ178- a producer of N-terminal fragment of human peroxyredoxin VI.

<150> RU 2003123534 (2003.29.07)

<210> 2

<211> 177

<212> cDNA-mRNA

<213> Homo sapiens

```

<400> cggttgcttg ctgtccacgc ggcgccccct catcacgcgc gcc atg ccc gga ggt ctg 58
      Met Pro Gly Gly Leu
      1 5
ctt ctc ggg gac gtg gct ccc aac ttt gag gcc aat acc acc gtc ggc 106
Leu Leu Gly Asp Val Ala Pro Asn Phe Gly Ala Asn Thr Thr Val Gly
      10 15 20
cgc atc cgt ttc cac gac ttt ctg gga gac tca tgg ggc att ctc ttc 154
Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser Trp Gly Ile Leu Phe
      25 30 35
tcc cac cct cgg gac ttt acc cca gtg tgc acc aca gag ctt ggc aga 202
Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr Thr Glu Leu Gly Arg
      40 45 50
gct gca aag ctg gca cca gaa ttt gcc aag agg aat gtt aag ttg att 250
Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg Asn Val Lys Leu Ile
      55 60 65
gcc ctt tca ata gac agt gtt gag gac cat ctt gcc tgg agc aag gat 298
Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu Ala Trp Ser Lys Asp
      70 75 80 85
atc aat gct tac aat tgt gaa gag ccc aca aag tta cct ttt ccc 346
Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu Lys Leu Pro Phe Pro
      90 95 100
atc atc gat gat agg aat cgg gag ctt gcc atc ctg ttg ggc atg ctg 394
Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile Leu Leu Gly Met Leu
      105 110 115
gat cca gca gag aag gat gaa aag ggc atg cct gtg aca gct cgt gtg 442
Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro Val Thr Ala Arg Val
      120 125 130

gtg ttt gtt ttt ggt cct gat aag aag ctg aag ctg tct atc ctc tac 490
Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys Leu Ser Ile Leu Tyr
      135 140 145
cca gct acc act ggc agg aac ttt gat gag att ctc agg gta gtc atc 538
Arg Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile Leu Arg Val Val Ile
      150 155 160 165

```

tct	ctc	cag	ctg	aca	gca	gaa	aaa	agg	gtt	gcc	acc
Ser	Leu	Gln	Leu	Thr	Ala	Glu	Lys	Arg	Val	Ala	Thr
170						175					

574

```

<210> 3
<211> 23
<212> primer_bind
<213> Artificial Sequence
<400> atcaccgtcc atatgccgg agg

<210> 4
<211> 25
<212> primer_bind
<213> Artificial Sequence
<400> ccagaattct taaggctggg gtgtg

<210> 5
<211> 27
<212> primer_bind
<213> Artificial Sequence
<400> gcgaaattaa tacgactcac tataggg

<210> 6
<211> 27
<212> primer_bind
<213> Artificial Sequence
<400> ccatccttcg aattcaactt aggtggc

```